



## SEQUENCE LISTING

#9

&lt;110&gt;Medlock et al.

&lt;120&gt; IL-17 Receptor Like Molecules and Uses Thereof

&lt;130&gt; 01017/36917A

&lt;140&gt; US 09/810,927

&lt;141&gt; 2001-03-16

&lt;150&gt; US 60/266,159

&lt;151&gt; 2001-02-02

&lt;150&gt; US 09/723,232

&lt;151&gt; 2000-11-27

&lt;150&gt; US 60/204,208

&lt;151&gt; 2000-05-12

&lt;150&gt; US 60/189,923

&lt;151&gt; 2000-03-08

&lt;160&gt; 27

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 1841

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;221&gt; CDS

&lt;222&gt; (50)..(1555)

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Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His	
485 490 495	
aaa tac gtg gtg gtc tac ttt aga gag att gat aca aaa gac gat tac	1594
Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr	
500 505 510 515	
aat gct ctc agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act	1642
Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr	
520 525 530	
gct ttc tgt gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga	1690
Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly	
535 540 545	
aaa aga tca caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccccc	1739
Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
550 555 560	
atgagaagca agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg	1799
atgatcctga agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac	1859
caataaaaatt ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat	1919
ttacaacttc aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta	1979
accattttga taatgcaaca ataaagcatc ttcagc	2015

<210> 5  
<211> 560

<212> PRT

<213> Homo sapiens

<400> 5

Met	Ser	Leu	Val	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala	Val	
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Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	Pro	
			20					25					30			
Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	Leu	
		35					40					45				
Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	Ile	
	50					55					60					
Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	Leu	
	65				70					75					80	
Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	Ser	
				85					90					95		
Tyr	Ser	Cys	Val	Arg	Leu	Glu	Cys	Ser	Gly	Ala	Ile	Met	Ala	Arg	Cys	
			100					105					110			
Asp	Leu	Asn	Leu	Leu	Gly	Ser	Ser	Asp	Arg	Ser	Ala	Ser	Ala	Ser	Arg	
		115					120					125				
Ala	Ala	Gly	Thr	Ala	Gly	Val	Gly	His	Gln	Thr	Trp	Leu	Ile	Phe	Val	
	130					135					140					
Val	Phe	Val	Glu	Gly	Gly	Phe	Thr	Val	Leu	Leu	Val	Leu	Asn	Ser	Ser	
	145				150					155					160	
Ala	Gln	Ala	Ile	Cys	Leu	Pro	Arg	Leu	Pro	Lys	Val	Leu	Gly	Leu	Gln	
				165					170					175		
Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val	Tyr	
			180					185					190			
Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp	Gly	
		195					200					205				
Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His	Ile	
	210					215					220					
Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp	Pro	
	225				230					235					240	
Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn	Phe	
				245					250					255		
Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His	Ser	
			260					265					270			
Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys	Gln	
		275					280					285				
Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly	Ala	
	290					295					300					

Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile  
 305 310 315 320  
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe  
 325 330 335  
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu  
 340 345 350  
 Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile Tyr  
 355 360 365  
 Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr  
 370 375 380  
 Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu Ile  
 385 390 395 400  
 Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn His  
 405 410 415  
 Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala  
 420 425 430  
 Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp  
 435 440 445  
 Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp Gly  
 450 455 460  
 Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu  
 465 470 475 480  
 Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile  
 485 490 495  
 His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys  
 500 505 510  
 Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys  
 515 520 525  
 Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val  
 530 535 540  
 Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser Leu  
 545 550 555 560

<210> 6  
 <211> 1713  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (273)..(1427)

<400> 6  
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 gctgctaagc ctggccgcgc tgtgcaggag cgccgtaccc cgagagccga ccgttcaatg 120

tggctctgaa actggggccat ctccagagtg gatgctacaa catgatctaa tcccggggaga														180
cttgaggggac ctccgagtag aacctgttac aactagtgtt gcaacaggggg actatttcaat														240
tttgatgaat gtaagctggg tactccgggc ag atg tgg aca ttt tcc tac atc Met Trp Thr Phe Ser Tyr Ile 1 5														293
ggc ttc cct gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn 10 15 20														341
att cct aat gca aat atg aat gaa gat ggc cct tcc atg tct gtg aat Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn 25 30 35														389
ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys 40 45 50 55														437
tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys 60 65 70														485
aag aat gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly 75 80 85														533
aac aga tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser 90 95 100														581
cag gtg ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val 105 110 115														629
att cca gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro 120 125 130 135														677
tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val 140 145 150														725
gtg ctc tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys 155 160 165														773
agc aag ccg gga ggc tgg ctg cct ctc ctc ctg ctg tct ctg ctg gtg Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val 170 175 180														821
gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu 185 190 195														869
agg atc aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile 200 205 210 215														917

aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att	965
Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile	
220 225 230	
tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	
tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt	1109
Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu	
265 270 275	
tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag	1157
Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu	
280 285 290 295	
ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac	1205
Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn	
300 305 310	
ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg	1253
Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val	
315 320 325	
gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc	1301
Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu	
330 335 340	
agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt	1349
Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys	
345 350 355	
gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca	1397
Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser	
360 365 370 375	
caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccacccc atgagaagca	1447
Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
380 385	
agagacctta aaggcttcct atcccaccaa ttacagggaa aaaacgtgtg atgatacctga	1507
agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaatt	1567
ttcaaataatt gctaactaat gtagcattaa ctaacgattg gaaaactacat ttacaacttc	1627
aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga	1687
taatgcaaca ataaagcatc ttcagc	1713

<210> 7  
 <211> 385  
 <212> PRT  
 <213> Homo sapiens

<400> 7

Met	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	Val	Glu	Leu	Asn	Thr	Val
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Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	Ala	Asn	Met	Asn	Glu	Asp
			20					25					30		
Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	Pro	Gly	Cys	Leu	Asp	His
		35					40					45			
Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	Trp	Asp
	50					55					60				
Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	Val	Asn
	65				70					75					80
Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	Gln	His
				85					90					95	
Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	Lys	Lys
			100					105					110		
Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	Glu	Gly
		115					120					125			
Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	Asp	Cys
	130					135					140				
Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	Val	Pro
145					150					155					160
Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu
				165					170					175	
Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	Val	Leu	Val	Ala	Gly	Ile
			180					185					190		
Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	Lys	Thr	Ser	Phe	Ser	Thr
		195					200					205			
Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	Val	Val	Tyr	Pro	Ser	Glu
	210					215					220				
Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	Thr	Glu	Phe	Leu	Gln	Asn
225					230					235					240
His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys	Ile
				245					250					255	
Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	Gln	Lys	Lys	Ala	Ala
			260					265					270		
Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	Asn	Ser	Val	Cys	Asp
		275					280					285			
Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser	Glu	Asn	Ser	Gln	Asp
	290					295					300				
Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	Asp	Leu	Arg	Ser	Gln
305					310					315					320
Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	Arg	Glu	Ile	Asp	Thr

325

330

335

Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met  
 340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln  
 355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser  
 370 375 380

Leu  
 385

<210> 8  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 2429-59

<400> 8  
 gcagacactg agagcattgt aatcg 25

<210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 1916-83

<400> 9  
 ggctcgtatg ttgtgtggaa ttgtgag 27

<210> 10  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR Primer  
 2429-56

<400> 10  
 atcaagaaga cttccttttc tac 23

<210> 11  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer 1916-80

<400> 11

tgcaaggcga ttaagttggg taacgccag

29

<210> 12  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 12  
gccgacgggg acgtggatga ac

22

<210> 13  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 13  
catgattacg ccaagctcta atacgactc

29

<210> 14  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nested PCR  
Primer

<400> 14  
cttcgccgag tgccctgtgca g

21

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Nest PCR  
Primer

<400> 15  
tcacgacgtt gtaaaacgac ggccagtg

28

<210> 16  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2469-50



<400> 16  
gcgatgtcgc tcgtgctgct aag

23

<210> 17  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer  
2469-54

<400> 17  
gcagcctggt gaggtgaaat tcac

24

<210> 18  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 18  
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

<210> 19  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Peptide

<400> 19  
Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg  
1 5 10 15

Arg Arg

<210> 20  
<211> 27  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Epogen signal  
peptide

<400> 20  
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu  
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly  
20 25

<210> 21  
 <211> 233  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide of Fc fragment

<400> 21

Glu	Pro	Lys	Ser	Ala	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	1	5	10	15
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	20	25	30	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	35	40	45	
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	50	55	60	
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	65	70	75	80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	85	90	95	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	100	105	110	
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	115	120	125	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	130	135	140	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	145	150	155	160
Asp	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	165	170	175	
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	180	185	190	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	195	200	205	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	210	215	220	
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								225	230		

<210> 22  
 <211> 644  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (159)..(641)

<400> 22

ctcaagtcac tccctaaaaa gacagtggaa ataaatttga ataaacaaaa caggcttgct 60  
gaaaataaaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggctgtcag 120  
tcagtgcctc acttgtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176  
Met Tyr Gln Val Val Ala  
1 5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224  
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser  
10 15 20

tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272  
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp  
25 30 35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320  
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His  
40 45 50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368  
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala  
55 60 65 70

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416  
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro  
75 80 85

cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta 464  
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu  
90 95 100

cag aca ggc tcc cac atg gac ccc cgg ggc aac tgc gag ctg ctc tac 512  
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr  
105 110 115

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc 560  
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly  
120 125 130

acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608  
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu  
135 140 145 150

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644  
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly  
155 160

<210> 23

<211> 161

<212> PRT

<213> Homo sapiens

<400> 23

Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr  
1 5 10 15

Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser  
20 25 30

Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro  
                   35                                  40                                  45  
 Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly  
                   50                                  55                                  60  
 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg  
                   65                                  70                                  75                                  80  
 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys  
                                   85                                  90                                  95  
 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly  
                                   100                                  105                                  110  
 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro  
                   115                                  120                                  125  
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg  
                   130                                  135                                  140  
 Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met  
                   145                                  150                                  155                                  160

Gly

<210> 24  
 <211> 521  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
                   1                                  5                                  10                                  15  
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
                                   20                                  25                                  30  
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
                   35                                  40                                  45  
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
                   50                                  55                                  60  
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
                   65                                  70                                  75                                  80  
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
                                   85                                  90                                  95  
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser  
                   100                                  105                                  110  
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn  
                   115                                  120                                  125  
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn  
                   130                                  135                                  140  
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu  
                   145                                  150                                  155                                  160

Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	Ala	Gly	Ser	Leu	165	170	175
Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	Glu	Thr	Val	Glu	180	185	190
Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	Met	Ala	Leu	Ile	195	200	205
Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro	His	Gln	210	215	220
Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr	Gly	Asp	Ser	225	230	235
Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	Thr	Cys	Gly	Ser	245	250	255
Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	Pro	Gln	Thr	Gly	260	265	270
Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	Gly	Gly	Trp	Leu	275	280	285
Pro	Ala	Ala	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	290	295	300
Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	305	310	315
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	325	330	335
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	340	345	350
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	355	360	365
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	370	375	380
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	385	390	395
Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	405	410	415
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	420	425	430
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	435	440	445
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	450	455	460
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	465	470	475
Phe	Phe	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	485	490	495

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 515 520

<210> 25

<211> 585

<212> PRT

<213> Homo sapiens

<400> 25

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val  
 1 5 10 15

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro  
 20 25 30

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu  
 35 40 45

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile  
 50 55 60

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu  
 65 70 75 80

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser  
 85 90 95

Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys  
 100 105 110

Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg  
 115 120 125

Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val  
 130 135 140

Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser  
 145 150 155 160

Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln  
 165 170 175

Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr  
 180 185 190

Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly  
 195 200 205

Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile  
 210 215 220

Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro  
 225 230 235 240

Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe  
 245 250 255

Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser  
 260 265 270

Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln  
 275 280 285  
 Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala  
 290 295 300  
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile  
 305 310 315 320  
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe  
 325 330 335  
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala  
 340 345 350  
 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 355 360 365  
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
 370 375 380  
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
 385 390 395 400  
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
 405 410 415  
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
 420 425 430  
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
 435 440 445  
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
 450 455 460  
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
 465 470 475 480  
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
 485 490 495  
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
 500 505 510  
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
 515 520 525  
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
 530 535 540  
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
 545 550 555 560  
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
 565 570 575  
 Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 580 585

<210> 26

<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 26  
cattttccta catcggttc cctg

24

<210> 27  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 27  
tgaatctggc ttctttcact gc

22